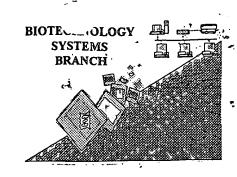
## RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/889,344Source: 09/889,344Date Processed by STIC: 9/29/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: <a href="mailto:patin21help@uspto.gov">patin21help@uspto.gov</a> or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: <a href="patin3help@uspto.gov">patin3help@uspto.gov</a> or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

## Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

BER KL

ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 09/88 4,599
ATTN: NEW RULES CASES	: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE
Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent outmission is saved in ASCII text.
5Variable Length.	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)  Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to Include the skipped sequences.
8Skipped Sequences (NEW RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number
9 Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing.  Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.  Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of Patentln version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
	en de la companya de La companya de la co
13Misuse of n	in can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001

PCT09

DATE: 07/27/2001

TIME: 19:16:25

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               Output Set: N:\CRF3\07272001\1889344.raw
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                                                    001-2
    7 <120> TITLE OF INVENTION: Method of Site Specific Labeling of
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   11 <130> FILE REFERENCE: P50892
₩/-> 13 <140> CURRENT APPLICATION NUMBER: US/09/889,344
                                                    Does Not Comply
                                                 Corrected Diskette Needed
   14 <141> CURRENT FILING DATE: 2001-07-16
   16 <150> PRIOR APPLICATION NUMBER: PCT/US00/01481
   17 <151> PRIOR FILING DATE: 2000-01-20
   19 <150> PRIOR APPLICATION NUMBER: US 60/117,327
   20 <151> PRIOR FILING DATE: 1999-01-22
   22 <160> NUMBER OF SEQ ID NOS: 16
   24 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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   27 <211> LENGTH: 5
   28 <212> TYPE: PRT
   29 <213> ORGANISM: Artificial Sequence
   31 <220> FEATURE:
   32 <223> OTHER INFORMATION: site-specific labeling sequence
                      sel item 9 on Eva Jumany Sheet
   34 <400> SEQUENCE: 1
     Gln Ser Lys Val
   36
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   39 <211> LENGTH: 207
   40 <212> TYPE: PRT
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   43 <220> FEATURE:
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          (1) and (7) can be selected from 0 to 100
   47 <400> SEQUENCE:
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      40
   54
      55
   56
      57
                    70
                                   75
      w--⊳ 58
                                90
  60
      Xaa Xaa Xaa Xaa Gln Ser Lys Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa
   61
              100
                             105
  62
      63
                          120
W--> 64\
      65
                       135
                                      140
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/889,344

sel dem 9 on Eva Sunnavy Hest RAW SEQUENCE LISTING DATE: 07/27/2001 PATENT APPLICATION: US/09/889,344 TIME: 19:16:25

Input Set : A:\USSEQLIST.TXT

Output Set: N:\CRF3\07272001\1889344.raw

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see idens 9 and 5

120 <400> SEQUENCE: 4

RAW SEQUENCE LISTING DATE: 07/27/2001 PATENT APPLICATION: US/09/889,344 TIME: 19:16:25

Input Set : A:\USSEQLIST.TXT

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RAW SEQUENCE LISTING DATE: 07/27/2001 PATENT APPLICATION: US/09/889,344 TIME: 19:16:25

Input Set : A:\USSEQLIST.TXT

Output Set: N:\CRF3\07272001\I889344.raw

186 <213> ORGANISM: Unknown 188 <220> FEATURE: 189 <223> OTHER INFORMATION: Oligonucleotide designed to introduce Q tag 191 <400> SEQUENCE: 10 192 tgtacctcag accatatgag cactatcgaa gaacgcg 37 194 <210> SEQ ID NO: 11 195 <211> LENGTH: 78 196 <212> TYPE: DNA 197 <213> ORGANISM: Unknown 199 <220> FEATURE: 200 <223> OTHER INFORMATION: Oligonucleotide designed to introduce Q tag 202 <400> SEQUENCE: 11 203 tqatqtcaqt caaqcttacq qacccqqcaq aactttqqac tqqqacaqqq acaqcqcctq 60 204 gtggccgttg atgtaatc 78 206 <210> SEQ ID NO: 12 207 <211> LENGTH: 12 208 <212> TYPE: PRT 209 <213> ORGANISM: Artificial Sequence 211 <220> FEATURE: 212 <223> OTHER INFORMATION: Derivative of E. coli ACP protein 214 <400> SEQUENCE: 12 215 Leu Ser Leu Ser Gln Ser Lys Val Leu Pro Gly Pro 216 218 <210> SEQ ID NO: 13 219 <211> LENGTH: 92 220 <212> TYPE: DNA 221 <213> ORGANISM: Unknown 223 <220> FEATURE: 224 <223> OTHER INFORMATION: Oligonucleotide designed to introduce Q tag into 225 Streptococcus haemophilus FabH gene 227 <400> SEQUENCE: 13 228 tatcatatga gcctgtccct gtcccagtcc aaagttctgc cgggtccggg taccctcgag 60 229 ggatccgctt ttgcaaaaat aagtcaggtt gc 92 231 <210> SEQ ID NO: 14 232 <211> LENGTH: 53 233 <212> TYPE: DNA 234 <213> ORGANISM: Unknown 236 <220> FEATURE: 237 <223> OTHER INFORMATION: Oligonucleotide designed to introduce Q tag into Streptococcus haemophilus FabH gene 240 <400> SEQUENCE: 14 241 ctcagatctg agctcactag tggatcctta aattgtaaga atgagcgtgc ccc 53 243 <210> SEQ ID NO: 15 244 <211> LENGTH: 364 245 <212> TYPE: PRT 246 <213> ORGANISM: Artificial Sequence 248 <220> FEATURE: 249 <223> OTHER INFORMATION: Modified sequence of Streptococus haemophilus FabH 251 <400> SEQUENCE: 15

## RAW SEQUENCE LISTING

PATENT APPLICATION: U3/49/389,344 DATE: 07/27/2001 TIME: 19:16:25

Input Set : A:\USSEQLIST.TXT

Output Set: N:\CRF3\07272001\1889344.raw

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252 Met Gly His His His His His His His His His Ser Ser Co
254
     Ile Glu Gly Arg His Met ser Lew Ser Lew Ser Gln S- Lys Val Lew
                                    25
256
     Pro Gly Pro Gly The Leu Glu Gly Ser Ala Phe Ala Lys Ile Ser Gln
257
     Val Ala Hiş Tyr Val Pro Glu Gln Val Val Thr Asn His Asp Leu Ala
258
259
     Gln Ile Met Asp Thr Asn Asp Glu Trp Ile common Thr Gly Ile
    Arg Gln Arg His Ile car Arg Thr Glu Ser Thr Ser Asp Leu Ala Thr
262
                                             ---- J
                ____55
    Glu Val Ala Lys Lys Leu Met Ala Lys Ala Gly Ile Thr Gly Lys Glu
264
265
                                    105
266
    Leu Asp Phe Ile Ile Leu Ala Thr Ile Thr Pro Asp Ser Met Met Pro
267
                                120
    Ser Thr Ala Ala Arg Val Gln Ala Asn Ile Gly Ala Asn Lys Ala Phe
268
                            135
    Ala Phe Asp Leu Thr Ala Ala Cys Ser Gly Phe Val Phe Ala Leu Ser
270
271
                       150
                                            155
    Thr Ala Glu Lys Phe Ile Ala Ser Gly Arg Phe Gln Lys Gly Leu Val
272
273
                    165
                                        170
    Ile Gly Ser Glu Thr Leu Ser Lys Ala Val Asp Trp Ser Asp Arg Ser
274
275
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                                   185
276
    Thr Ala Val Leu Phe Gly Asp Gly Ala Gly Gly Val Leu Leu Glu Ala
                                200
    Ser Glu Gln Glu His Phe Leu Ala Glu Ser Leu Asn Ser Asp Gly Ser
278
279
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    Arg Ser Glu Cys Leu Thr Tyr Gly His Ser Gly Leu His Ser Pro Phe
280
281
                        230
                                            235
    Ser Asp Gln Glu Ser Ala Asp Ser Phe Leu Lys Met Asp Gly.Arg Thr
282
283
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    Val Phe Asp Phe Ala Ile Arg Asp Val Ala Lys Ser Ile Lys Gln Thr
285
               260
                                    265
    Ile Asp Glu Ser Pro Ile Glu Val Thr Asp Leu Asp Tyr Leu Leu Leu
286
                               280
    His Gln Ala Asn Asp Arg Ile Leu Asp Lys Met Ala Arg Lys Ile Gly
288
289
                            295
                                                300
290 Val Asp Arg Ala Lys Leu Pro Ala Asn Met Met Glu Tyr Gly Asn Thr
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292 Ser Ala Ala Ser Ile Pro Ile Leu Leu Ser Glu Cys Val Glu Gln Gly
293
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                                        330
294 Leu Ile Pro Leu Asp Gly Ser Gln Thr Val Leu Leu Ser Gly Phe Gly
295
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300 <211> LENGTH: 503
301 <212> TYPE: PRT
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VERIFICATION SUMMARY DATE: 07/27/2001 PATENT APPLICATION: US/09/889,344 TIME: 19:16:26

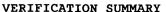
Input Set : A:\USSEQLIST.TXT

Output Set: N:\CRF3\07272001\1889344.raw

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L:87 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3

DATE: 07/27/2001



PATENT APPLICATION: US/09/889,344 TIME: 19:16:26

Input Set : A:\USSEQLIST.TXT

Output Set: N:\CRF3\07272001\1889344.raw

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